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TECH CENTER 1600/2900

1647

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/292,862A

DATE: 05/01/2001
TIME: 17:57:52

Input Set : A:\PTO.txt
Output Set : N:\CRF3\05012001\I292862A.raw

ENTERED

4 <110> APPLICANT: Walter, Michael A.
5 Jordan, Tim
6 Raymond, Vincent
8 <120> TITLE OF INVENTION: NOVEL MUTATIONS IN THE FREAC3 GENE FOR
9 DIAGNOSIS AND PROGNOSIS OF GLAUCOMA AND ANTERIOR SEGMENT
10 DYSGENESIS
12 <130> FILE REFERENCE: 07540/020003
14 <140> CURRENT APPLICATION NUMBER: US 09/292,862A
15 <141> CURRENT FILING DATE: 1999-04-16
17 <150> PRIOR APPLICATION NUMBER: 60/084,784
18 <151> PRIOR FILING DATE: 1998-05-08
20 <150> PRIOR APPLICATION NUMBER: 60/082,206
21 <151> PRIOR FILING DATE: 1998-04-17
23 <160> NUMBER OF SEQ ID NOS: 12
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1978
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
32 <400> SEQUENCE: 1
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34 cccggcccgcg actcggactc ggcggccggc gcggcgccgc cccggcccgc cgagggtggg 120
35 gggcgggcggg cggcgcgggg cggcgcgag cgggggcccgc gcagcgcggc tactccgtgt 180
36 ccagccccc aa ctccctggga gtggtgccct acctcgccgc cgagcagagc tactaccgcg 240
37 cggcgggcggc ggcggccggg ggcggctaca ccgccatgcc ggcccccatg agcgtgtact 300
38 cgcaccctgc gcacgcccag cagtaccgcg gcggcatggc ccgcgcctac gggccctaca 360
39 cgccgcagcc gcagcccaag gacatggtga agccgcccta tagctacatc gcgtcatca 420
40 ccatggccat ccagaacgcc ccggacaaga agatcacctc gaacggcatc taccagttca 480
41 tcatggaccg cttccccttc taccgggaca acaagcaggg ctggcagaac agcatccgcc 540
42 acaacctctc gctcaacgag tgcttcgtca aggtgccgcg cgacgacaag aagccgggca 600
43 agggcagcta ctggacgctg gacccggact cctacaacat gttcgagaac ggcagcttcc 660
44 tgcggcgggc gcggcgcttc aagaagaagg acgcgttgaa ggacaaggag gagaaggaca 720
45 ggcgtgcacct caaggagccg ccccccgcgc gcgccagccc ccgcccggcg ccgcccggagc 780
46 agggcgacgg caacgcgcgc ggtccgcagc cgccgcccgt gcgcattccg gacatcaaga 840
47 ccgagaacgg tacgtgcccc tcgcgcgcgc agcccctgtc cccggccgcc gccttgggca 900
48 gcggcagcgc cgccgcggtg cccaagatcg agagcccga cagcagcagc agcagcctgt 960
49 ccagcgggag cagcccccg ggcagccctgc cgtcggcgcg gccgctcagc ctggacgggtg 1020
50 cggattccgc gccgcgcgc cccgcgcctc ccgcccgcgc gccgcacat agccagggt 1080
51 tcagcgtgga caacatcatg acgtcgtgc ggggggtcgcc gcagagcgcg gccgcggagc 1140
52 tcagctccgg cttcttgccc tcggcgggcg cgtcctcgcg cgcggggatc gcacccccgc 1200
53 tggcgctcgg cgccctactc ccgggccaga gctccctcta cagctcccc tgacgacaga 1260
54 cctccagcgc gggcagctcg ggcggcgcg gcggcgcgcg gggggccgcg gggggcgcg 1320
55 gcggcgccgc gacctaccac tgcaacctgc aagccatgag cctgtacgcg gccggcgagc 1380
56 gcgggggcca cttgcagggc gcgcccgggg gcggcgcgcg ctcggcgctg gacgaccccc 1440
57 tgcccgacta ctctctgcct ccggtcacca cagcagctc gtcgtccctg agtcacggcg 1500
58 gcggcgggcg cggcgcgggg ggaggccagg aggcgggcca ccacctgcg gccaccaag 1560
59 gccgcctcac ctcgtgttac ctgaaccagg cggggcggaga cctggggcac ttggcgagcg 1620

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60 cggcgccggc ggcggcgcc gcaggctacc cgggccagca gcagaacttc cactcggtgc 1680
61 gggagatggt cgagtcacag aggatcggtc tgaacaactc tccagtgaac gggaatagta 1740
62 gctgtcaaat ggccttccct tccagccagt ctctgtaccg cacgtccgga gctttcgtct 1800
63 acgactgtag caagtgttga cacaccctca aagccgaact aaatcgaacc ccaaagcagg 1860
64 aaaagctaaa ggaacccatc aaggcaaat cgaaactaaa aaaaaaaaaat ccaattaaaa 1920
65 aaaacccctg agaattattca ccacaccagc gaacagaata tccctccaaa aattcagc 1978
67 <210> SEQ ID NO: 2
68 <211> LENGTH: 553
69 <212> TYPE: PRT
70 <213> ORGANISM: Homo sapiens
72 <400> SEQUENCE: 2
73 Met Gln Ala Arg Tyr Ser Val Ser Ser Pro Asn Ser Leu Gly Val Val
74 1 5 10 15
75 Pro Tyr Leu Gly Gly Glu Gln Ser Tyr Tyr Arg Ala Ala Ala Ala Ala
76 20 25 30
77 Ala Gly Gly Gly Tyr Thr Ala Met Pro Ala Pro Met Ser Val Tyr Ser
78 35 40 45
79 His Pro Ala His Ala Glu Gln Tyr Pro Gly Gly Met Ala Arg Ala Tyr
80 50 55 60
81 Gly Pro Tyr Thr Pro Gln Pro Gln Pro Lys Asp Met Val Lys Pro Pro
82 65 70 75 80
83 Tyr Ser Tyr Ile Ala Leu Ile Thr Met Ala Ile Gln Asn Ala Pro Asp
84 85 90 95
85 Lys Lys Ile Thr Leu Asn Gly Ile Tyr Gln Phe Ile Met Asp Arg Phe
86 100 105 110
87 Pro Phe Tyr Arg Asp Asn Lys Gln Gly Trp Gln Asn Ser Ile Arg His
88 115 120 125
89 Asn Leu Ser Leu Asn Glu Cys Phe Val Lys Val Pro Arg Asp Asp Lys
90 130 135 140
91 Lys Pro Gly Lys Gly Ser Tyr Trp Thr Leu Asp Pro Asp Ser Tyr Asn
92 145 150 155 160
93 Met Phe Glu Asn Gly Ser Phe Leu Arg Arg Arg Arg Phe Lys Lys
94 165 170 175
95 Lys Asp Ala Leu Lys Asp Lys Glu Glu Lys Asp Arg Leu His Leu Lys
96 180 185 190
97 Glu Pro Pro Pro Pro Gly Ala Ser Pro Arg Pro Ala Pro Pro Glu Gln
98 195 200 205
99 Ala Asp Gly Asn Ala Pro Gly Pro Gln Pro Pro Pro Val Arg Ile Gln
100 210 215 220
101 Asp Ile Lys Thr Glu Asn Gly Thr Cys Pro Ser Pro Pro Gln Pro Leu
102 225 230 235 240
103 Ser Pro Ala Ala Ala Leu Gly Ser Gly Ser Ala Ala Ala Val Pro Lys
104 245 250 255
105 Ile Glu Ser Pro Asp Ser Ser Ser Ser Ser Leu Ser Ser Gly Ser Ser
106 260 265 270
107 Pro Pro Gly Ser Leu Pro Ser Ala Arg Pro Leu Ser Leu Asp Gly Ala
108 275 280 285
109 Asp Ser Ala Pro Pro Pro Pro Ala Pro Ser Ala Pro Pro Pro His His
110 290 295 300

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```

111 Ser Gln Gly Phe Ser Val Asp Asn Ile Met Thr Ser Leu Arg Gly Ser
112 305 310 315 320
113 Pro Gln Ser Ala Ala Glu Leu Ser Ser Gly Leu Leu Ala Ser Ala
114 325 330 335
115 Ala Ala Ser Ser Arg Ala Gly Ile Ala Pro Pro Leu Ala Leu Gly Ala
116 340 345 350
117 Tyr Ser Pro Gly Gln Ser Ser Leu Tyr Ser Ser Pro Cys Ser Gln Thr
118 355 360 365
119 Ser Ser Ala Gly Ser Ser Gly Gly Gly Gly Ala Gly Ala Ala
120 370 375 380
121 Gly Gly Ala Gly Gly Ala Gly Thr Tyr His Cys Asn Leu Gln Ala Met
122 385 390 395 400
123 Ser Leu Tyr Ala Ala Gly Glu Arg Gly Gly His Leu Gln Gly Ala Pro
124 405 410 415
125 Gly Gly Ala Gly Gly Ser Ala Val Asp Asp Pro Leu Pro Asp Tyr Ser
126 420 425 430
127 Leu Pro Pro Val Thr Ser Ser Ser Ser Ser Ser Leu Ser His Gly Gly
128 435 440 445
129 Gly Gly Gly Gly Gly Gly Gly Gln Glu Ala Gly His His Pro Ala
130 450 455 460
131 Ala His Gln Gly Arg Leu Thr Ser Trp Tyr Leu Asn Gln Ala Gly Gly
132 465 470 475 480
133 Asp Leu Gly His Leu Ala Ser Ala Ala Ala Ala Ala Ala Ala Gly
134 485 490 495
135 Tyr Pro Gly Gln Gln Gln Asn Phe His Ser Val Arg Glu Met Phe Glu
136 500 505 510
137 Ser Gln Arg Ile Gly Leu Asn Asn Ser Pro Val Asn Gly Asn Ser Ser
138 515 520 525
139 Cys Gln Met Ala Phe Pro Ser Ser Gln Ser Leu Tyr Arg Thr Ser Gly
140 530 535 540
141 Ala Phe Val Tyr Asp Cys Ser Lys Phe
142 545 550
145 <210> SEQ ID NO: 3
146 <211> LENGTH: 12
147 <212> TYPE: DNA
148 <213> ORGANISM: Homo sapiens
150 <400> SEQUENCE: 3
151 agtaaataaa ca 12
153 <210> SEQ ID NO: 4
154 <211> LENGTH: 12
155 <212> TYPE: DNA
156 <213> ORGANISM: Homo sapiens
158 <400> SEQUENCE: 4
159 agtaaacaaa ca 12
161 <210> SEQ ID NO: 5
162 <211> LENGTH: 20
163 <212> TYPE: DNA
164 <213> ORGANISM: Homo sapiens
166 <400> SEQUENCE: 5

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167 gcttcattcc gaatcaccag                                20
169 <210> SEQ ID NO: 6
170 <211> LENGTH: 20
171 <212> TYPE: DNA
172 <213> ORGANISM: Homo sapiens
174 <400> SEQUENCE: 6
175 gtccctcccc tccaactatc                                20
177 <210> SEQ ID NO: 7
178 <211> LENGTH: 13
179 <212> TYPE: DNA
180 <213> ORGANISM: Homo sapiens
182 <400> SEQUENCE: 7
183 gcccccgccg atg                                       13
185 <210> SEQ ID NO: 8
186 <211> LENGTH: 13
187 <212> TYPE: DNA
188 <213> ORGANISM: Homo sapiens
190 <400> SEQUENCE: 8
191 ggccgcccgc atg                                       13
193 <210> SEQ ID NO: 9
194 <211> LENGTH: 12
195 <212> TYPE: DNA
196 <213> ORGANISM: Homo sapiens
198 <400> SEQUENCE: 9
199 gggatatcga tg                                       12
201 <210> SEQ ID NO: 10
202 <211> LENGTH: 12
203 <212> TYPE: DNA
204 <213> ORGANISM: Homo sapiens
206 <400> SEQUENCE: 10
207 gggatatgga tg                                       12
209 <210> SEQ ID NO: 11
210 <211> LENGTH: 12
211 <212> TYPE: DNA
212 <213> ORGANISM: Homo sapiens
214 <400> SEQUENCE: 11
215 agtagtggtta cc                                       12
217 <210> SEQ ID NO: 12
218 <211> LENGTH: 12
219 <212> TYPE: DNA
220 <213> ORGANISM: Homo sapiens
222 <400> SEQUENCE: 12
223 agtactggta cc                                       12

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VERIFICATION SUMMARY

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